wwPDB EM Validation Summary Report (i)

Nov 9, 2022 – 03:39 AM JST

PDB ID	:	6AJ9
EMDB ID	:	EMD-9634
Title	:	The structure of Enterovirus D68 mature virion in complex with Fab 15C5 and 11G1
Authors	:	Zheng, Q.B.; Zhu, R.; Xu, L.F.; He, M.Z.; Yan, X.D.; Cheng, T.; Li, S.W.
Deposited on	:	2018-08-27
Resolution	:	3.50 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (i)) were used in the production of this report:

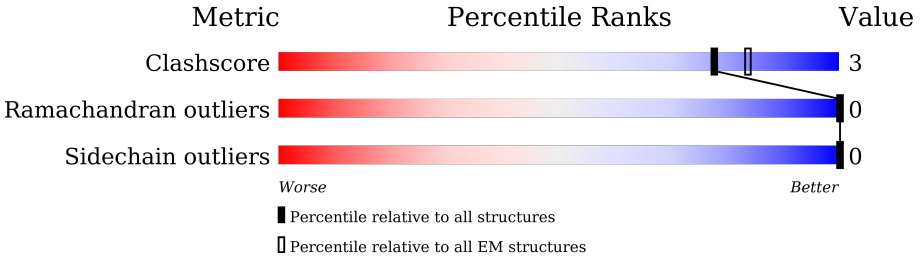
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	E	113	53%, 85%, 15%
2	D	122	20%, 80%, 6%, 14%
3	L	107	6%, 82%, 8%, 9%
4	H	116	·, 94%, 6%
5	A	295	·, 71%, ·, 25%
6	B	248	7%, 86%, 8%, 6%
7	C	247	·, 87%, 5%, 8%

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 8694 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called VL of Fab 11G1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	E	113	889	565	142	178	4	0	0

- Molecule 2 is a protein called VH of Fab 11G1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	D	105	814	516	131	161	6	0	0

- Molecule 3 is a protein called VL of Fab 15C5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	L	97	741	464	123	150	4	0	0

- Molecule 4 is a protein called VH of Fab 15C5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	H	116	919	585	151	178	5	0	0

- Molecule 5 is a protein called Capsid protein VP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	A	221	1763	1138	302	317	6	0	0

- Molecule 6 is a protein called Capsid protein VP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	B	233	1831	1170	317	332	12	0	0

- Molecule 7 is a protein called Capsid protein VP3.

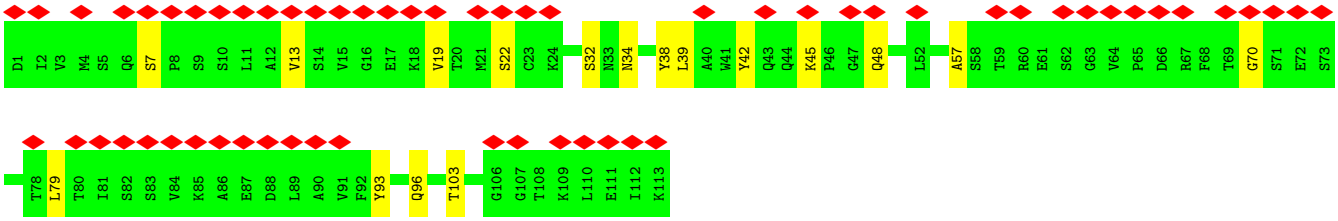
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	C	227	1737	1100	284	336	17	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

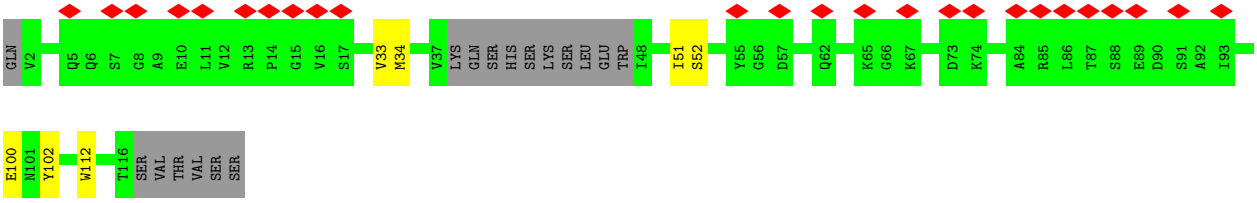
- Molecule 1: VL of Fab 11G1

Chain E:



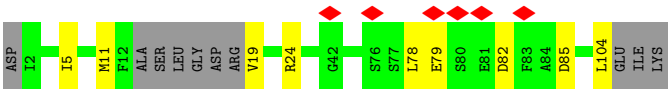
- Molecule 2: VH of Fab 11G1

Chain D:



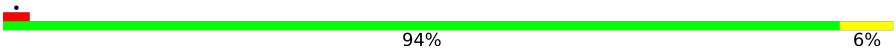
- Molecule 3: VL of Fab 15C5

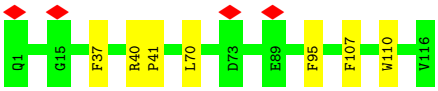
Chain L:



- Molecule 4: VH of Fab 15C5

Chain H:





- Molecule 5: Capsid protein VP1

Chain A: 71% 25%

ILE GLU SER ILE ILE LYS THR ALA THR ASP THR VAL LYS SER GLU ILE ASN ALA GLU LEU GLY VAL VAL PRO SER LEU ASN ALA VAL GLU THR GLY ALA THR SER ASN THR GLU PRO GLU GLU A42 R46 I95 L103 R104 R105 V125 A126 V127 N128 GLY SER GLY ASN ASN

T134 T154 D159 F203 E204 K205 N206 N212 D215 N219 T234 K242 Y267 LYS GLY LYS GLU ARG ALA PRO ASN ALA LEU ASN ALA ILE ILE GLY ASN ARG ASP SER VAL LYS THR MET PRO HIS ASN ILE VAL

- Molecule 6: Capsid protein VP2

Chain B: 7% 86% 8% 6%

SER PRO SER ALA GLU ALA CYS GLY TYR SER ASP ARG VAL L14 Q15 N20 T25 Q26 E27 A28 A29 N30 Y31 C32 C33 A34 E37 H45 E46 I50 D51 K52 E57 T58 D61 R62 L82 I89 G90 M91 I108 E150 T171 R181 I188 V189

L190 P191 D199 H204 T222 R243 H244 A245 I246 THR GLN

- Molecule 7: Capsid protein VP3

Chain C: 87% 5% 8%

G1 D17 E50 T75 Q79 Q89 R95 R104 Y105 L113 F157 G158 R176 MET PHE ASN ASN ASP ALA LYS S184 T185 N186 A187 I216 G234 GLN LEU ASP HIS LEU HIS ALA ALA GLU ALA ALA TYR GLN

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	102512	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	25	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.262	Depositor
Minimum map value	-0.155	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.0339	Depositor
Map size (Å)	676.8, 676.8, 676.8	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.128, 1.128, 1.128	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
1	E	0.29	0/911	0.55	0/1235
2	D	0.32	0/831	0.56	0/1121
3	L	0.31	0/755	0.60	0/1018
4	H	0.37	0/946	0.52	0/1281
5	A	0.40	0/1810	0.60	2/2462 (0.1%)
6	B	0.39	0/1889	0.61	1/2587 (0.0%)
7	C	0.36	0/1777	0.57	0/2421
All	All	0.36	0/8919	0.58	3/12125 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	A	103	LEU	CA-CB-CG	5.19	127.24	115.30
5	A	95	ILE	CG1-CB-CG2	-5.12	100.14	111.40
6	B	37	GLU	C-N-CA	5.08	134.40	121.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	889	0	856	10	0
2	D	814	0	775	4	0
3	L	741	0	713	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	H	919	0	859	4	0
5	A	1763	0	1751	9	0
6	B	1831	0	1762	14	0
7	C	1737	0	1702	10	0
All	All	8694	0	8418	49	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

The worst 5 of 49 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:32:SER:HB3	5:A:159:ASP:O	1.81	0.81
6:B:20:ASN:HB3	6:B:62:ARG:HD3	1.70	0.73
6:B:62:ARG:NH2	6:B:91:MET:SD	2.72	0.63
4:H:40:ARG:HH21	4:H:41:PRO:HD2	1.65	0.61
1:E:42:TYR:HB2	1:E:93:TYR:HB2	1.83	0.61

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	111/113 (98%)	104 (94%)	7 (6%)	0	100	100
2	D	101/122 (83%)	92 (91%)	9 (9%)	0	100	100
3	L	93/107 (87%)	87 (94%)	6 (6%)	0	100	100
4	H	114/116 (98%)	110 (96%)	4 (4%)	0	100	100
5	A	217/295 (74%)	198 (91%)	19 (9%)	0	100	100
6	B	231/248 (93%)	201 (87%)	30 (13%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	C	223/247 (90%)	213 (96%)	10 (4%)	0	100	100
All	All	1090/1248 (87%)	1005 (92%)	85 (8%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	100/100 (100%)	100 (100%)	0	100	100
2	D	87/104 (84%)	87 (100%)	0	100	100
3	L	84/92 (91%)	84 (100%)	0	100	100
4	H	96/96 (100%)	96 (100%)	0	100	100
5	A	192/253 (76%)	192 (100%)	0	100	100
6	B	197/209 (94%)	197 (100%)	0	100	100
7	C	200/215 (93%)	200 (100%)	0	100	100
All	All	956/1069 (89%)	956 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
7	C	79	GLN
7	C	188	ASN
1	E	96	GLN
2	D	5	GLN
2	D	6	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

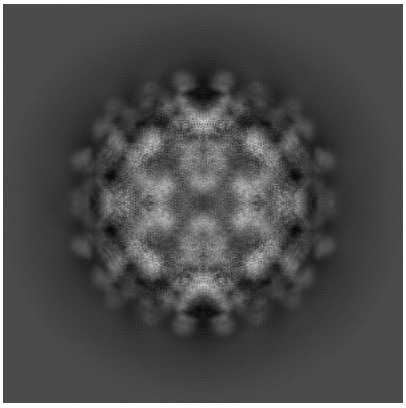
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-9634. These allow visual inspection of the internal detail of the map and identification of artifacts.

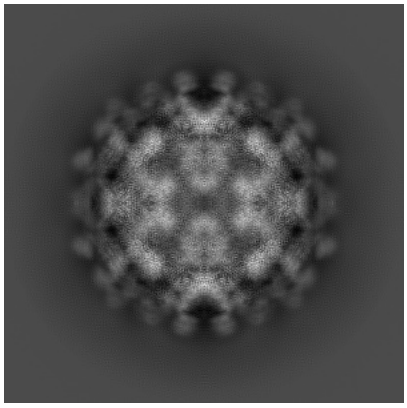
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

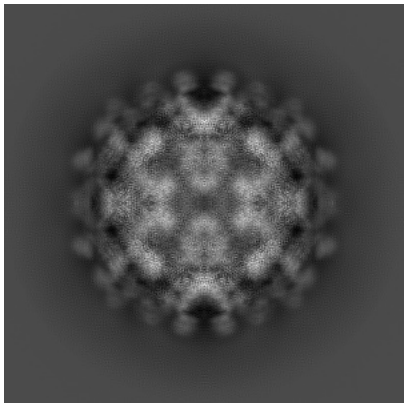
6.1.1 Primary map



X



Y

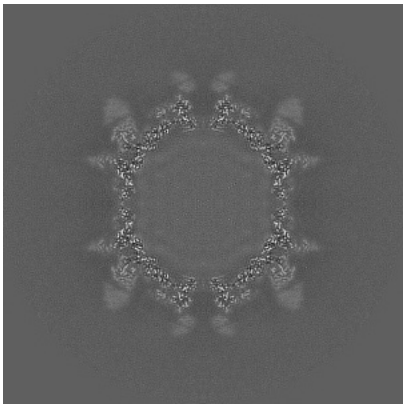


Z

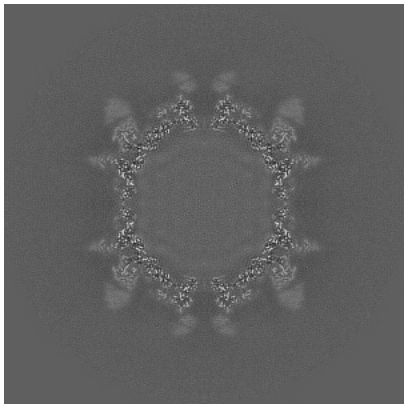
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

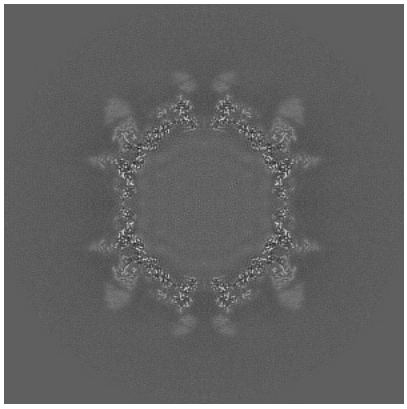
6.2.1 Primary map



X Index: 300



Y Index: 300

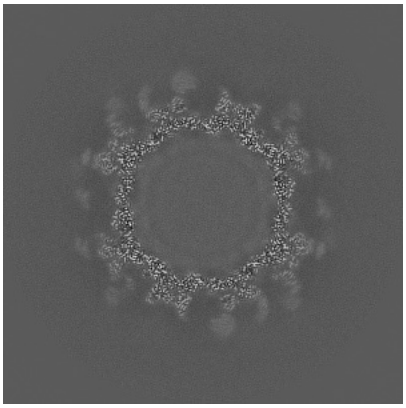


Z Index: 300

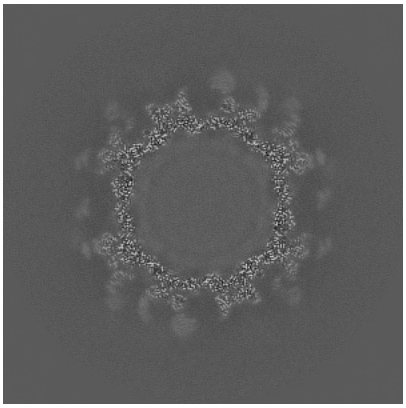
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

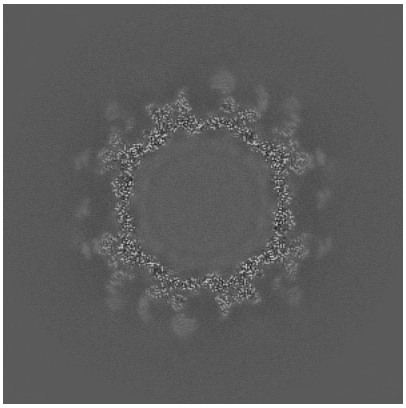
6.3.1 Primary map



X Index: 314



Y Index: 286

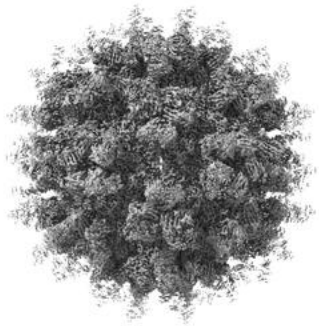


Z Index: 286

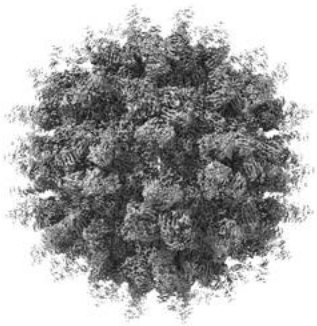
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views (i)

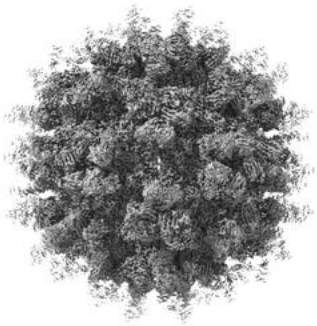
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0339. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

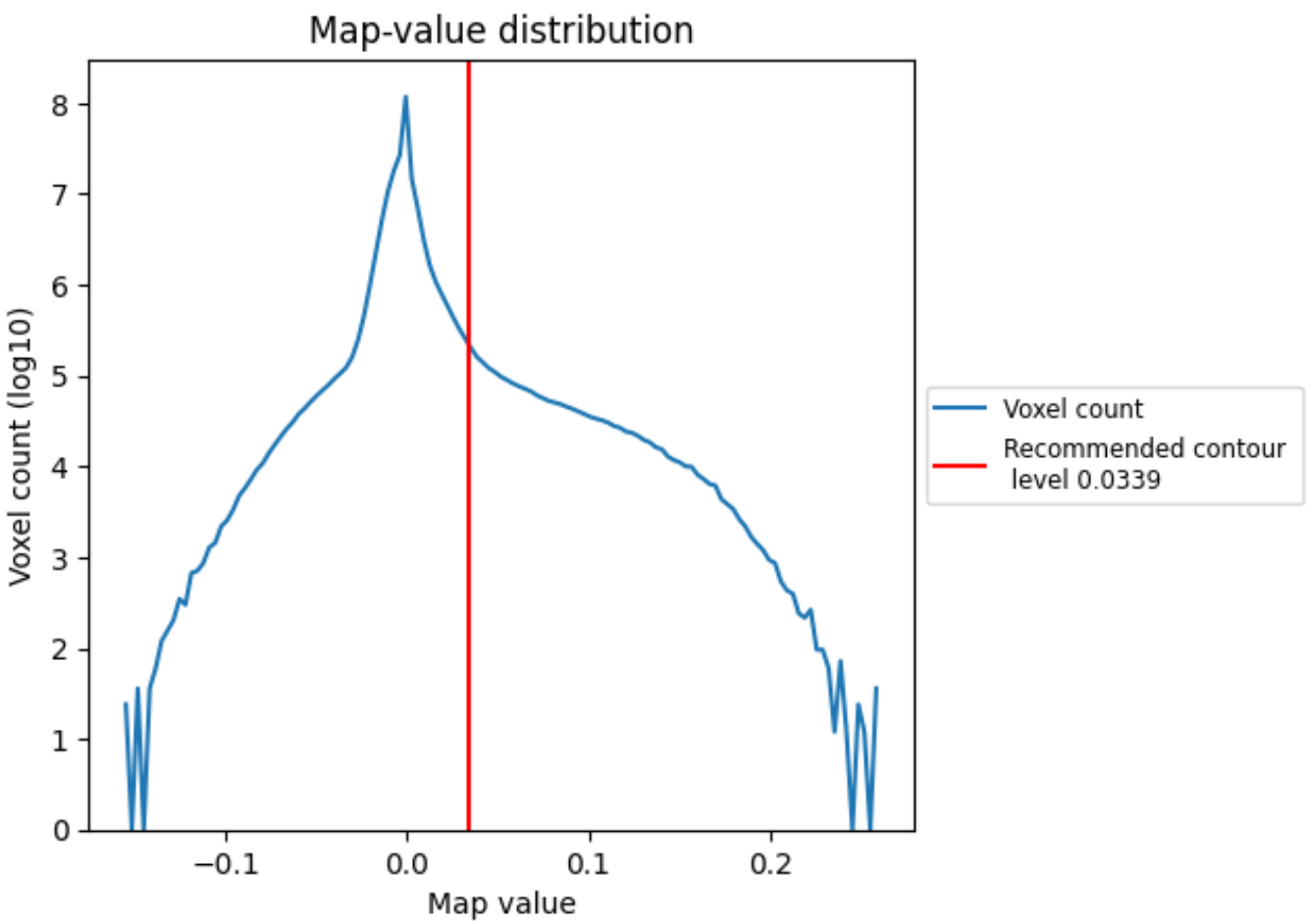
6.5 Mask visualisation (i)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis (i)

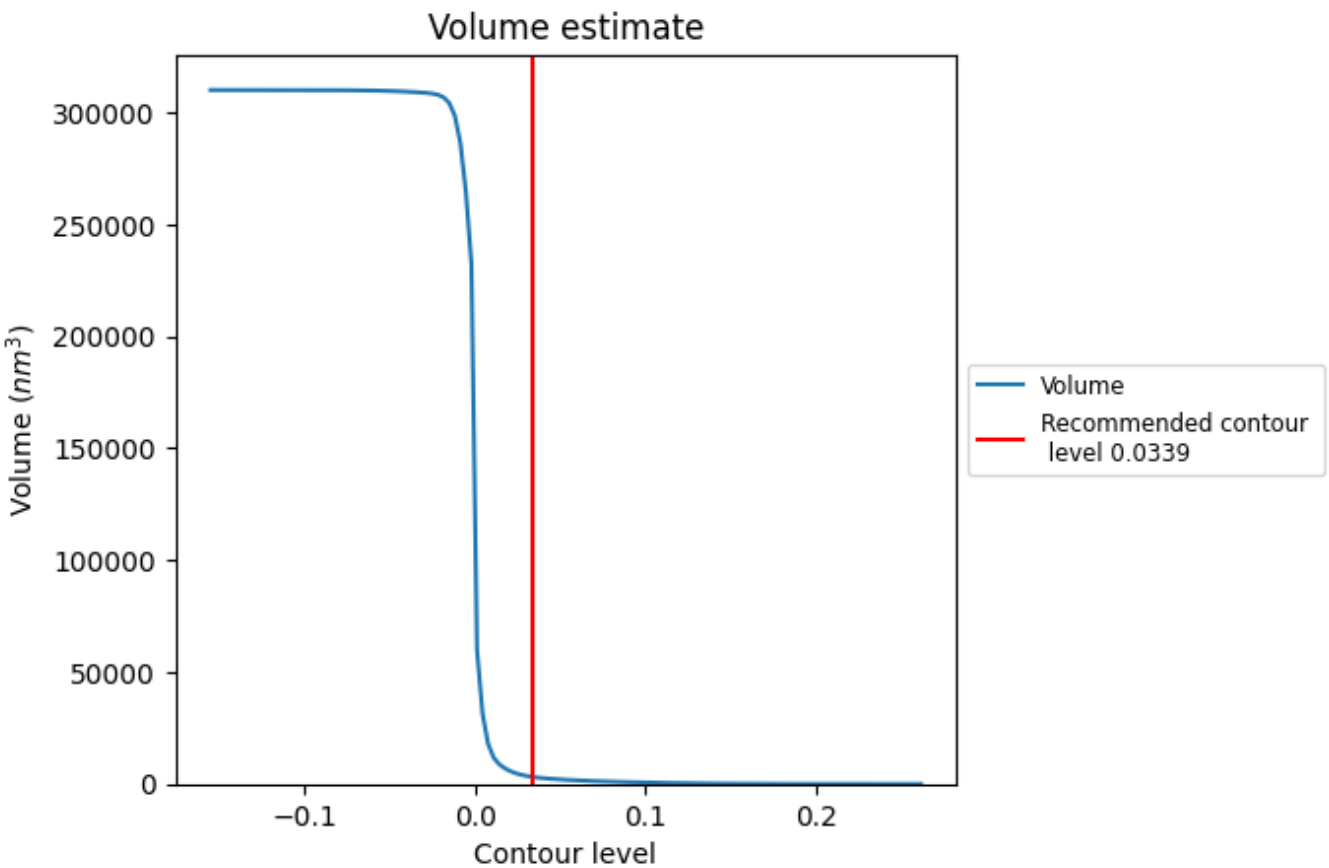
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

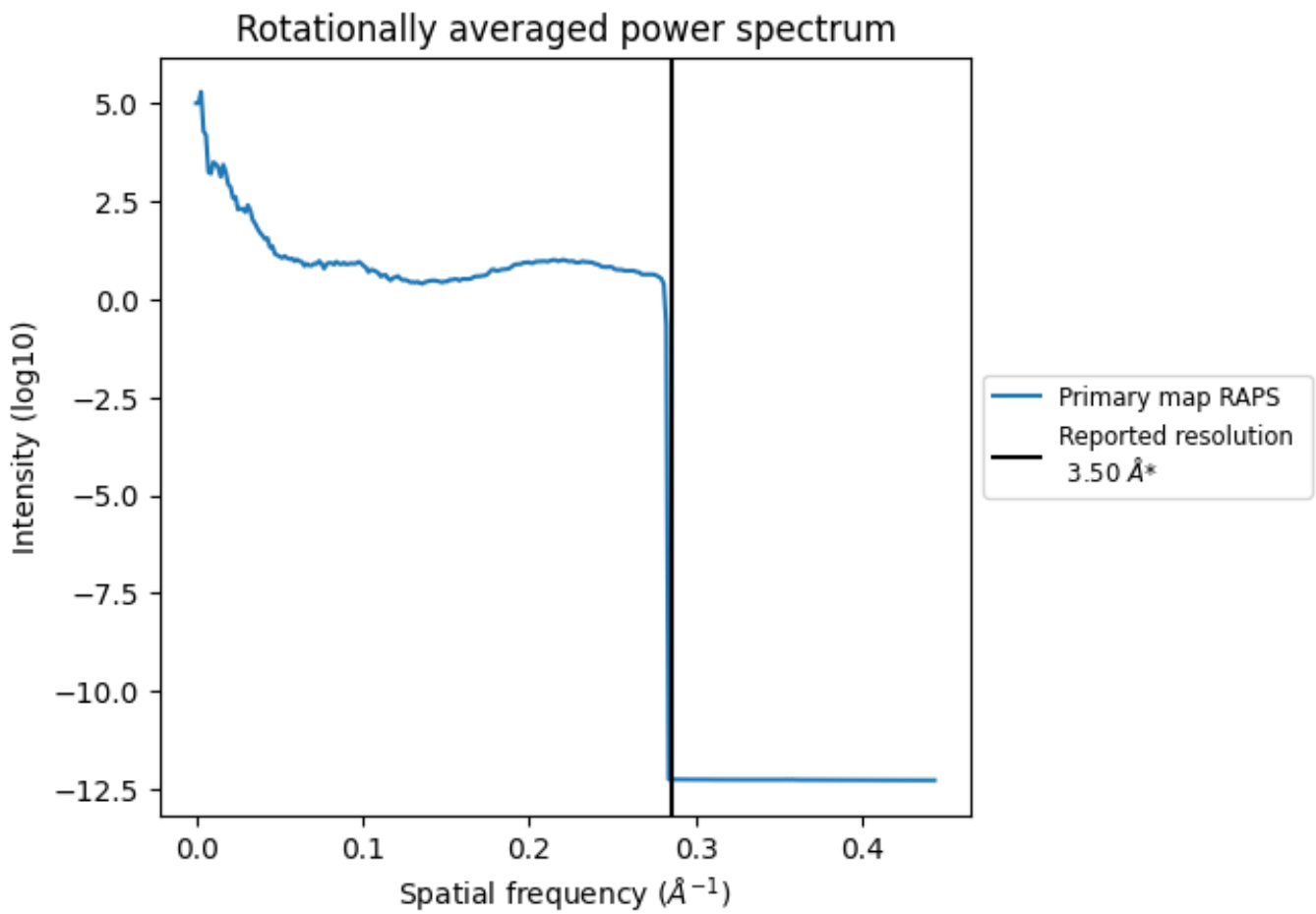
7.2 Volume estimate (i)



The volume at the recommended contour level is 3139 nm^3; this corresponds to an approximate mass of 2836 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)

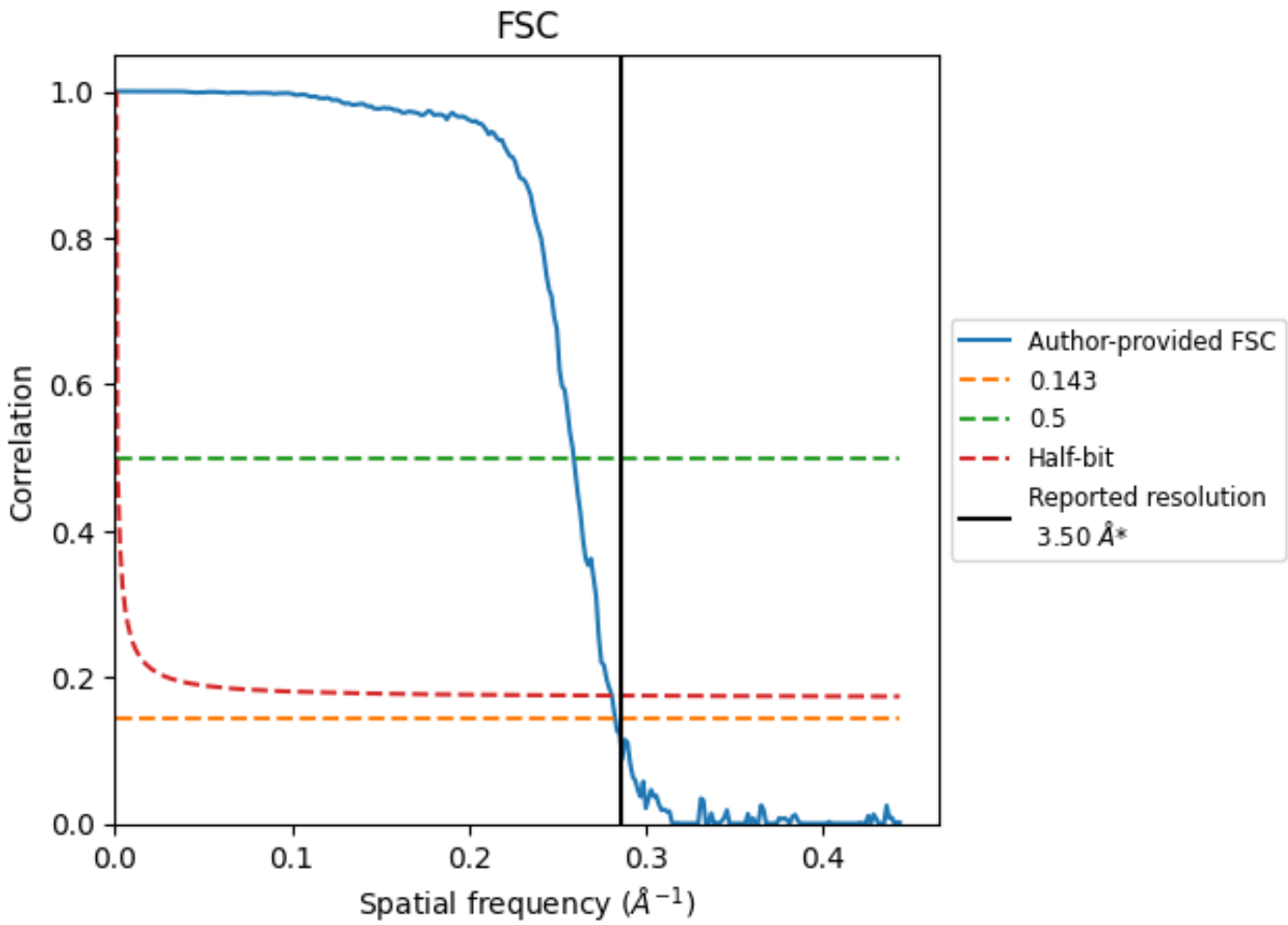


*Reported resolution corresponds to spatial frequency of 0.286 Å^{-1}

8 Fourier-Shell correlation (i)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC (i)



*Reported resolution corresponds to spatial frequency of 0.286 Å^{-1}

8.2 Resolution estimates (i)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.54	3.86	3.56
Unmasked-calculated*	-	-	-

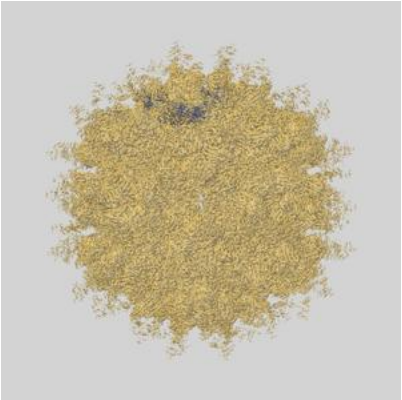
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit (i)

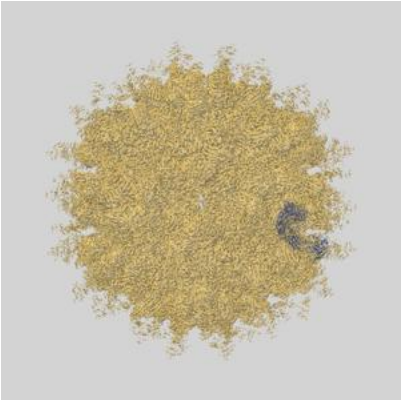
This section contains information regarding the fit between EMDB map EMD-9634 and PDB model 6AJ9. Per-residue inclusion information can be found in section 3 on page 5.

9.1 Map-model overlays

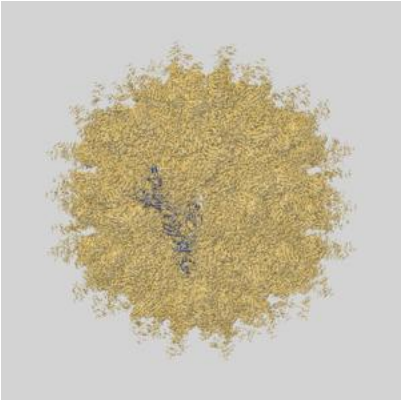
9.1.1 Map-model overlay (i)



X

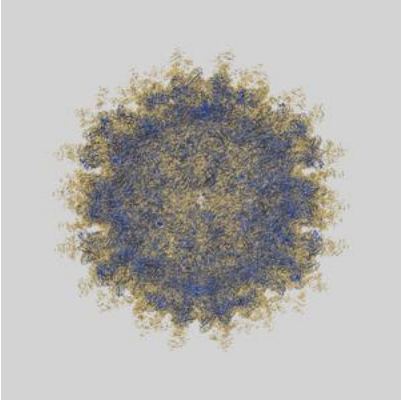


Y

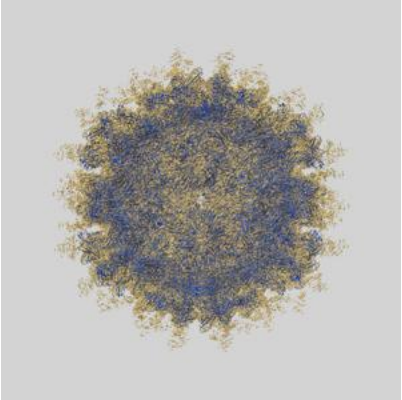


Z

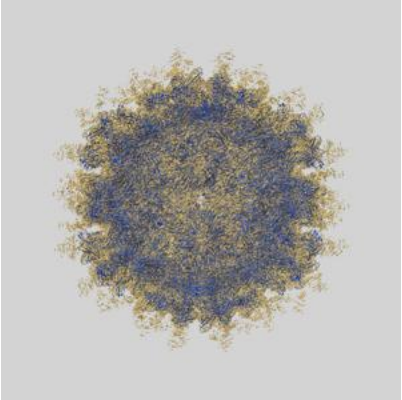
9.1.2 Map-model assembly overlay (i)



X



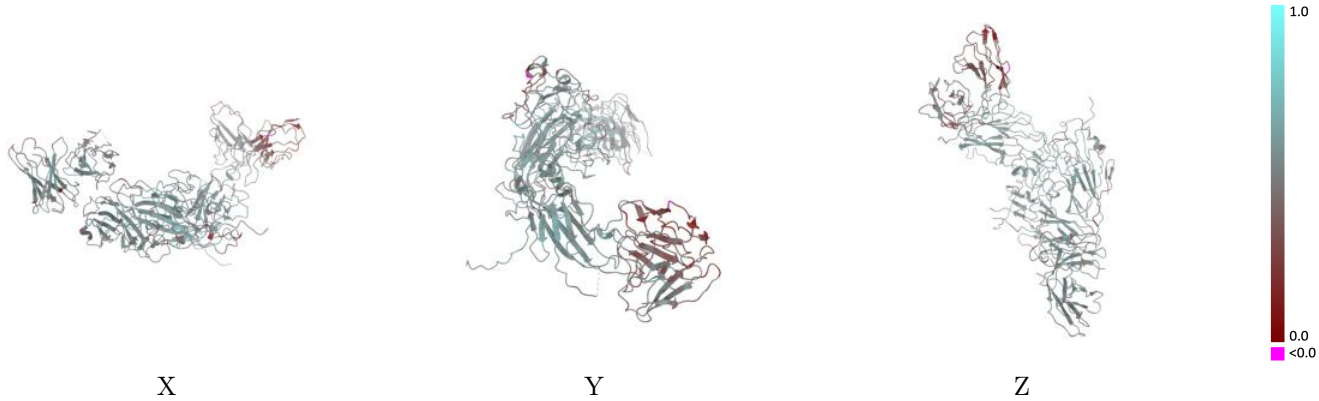
Y



Z

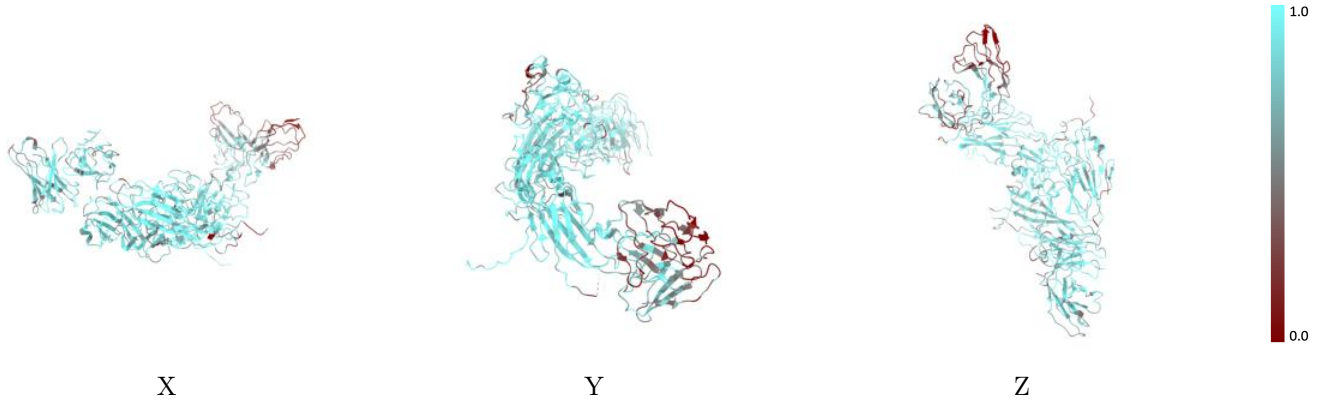
The images above show the 3D surface view of the map at the recommended contour level 0.0339 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



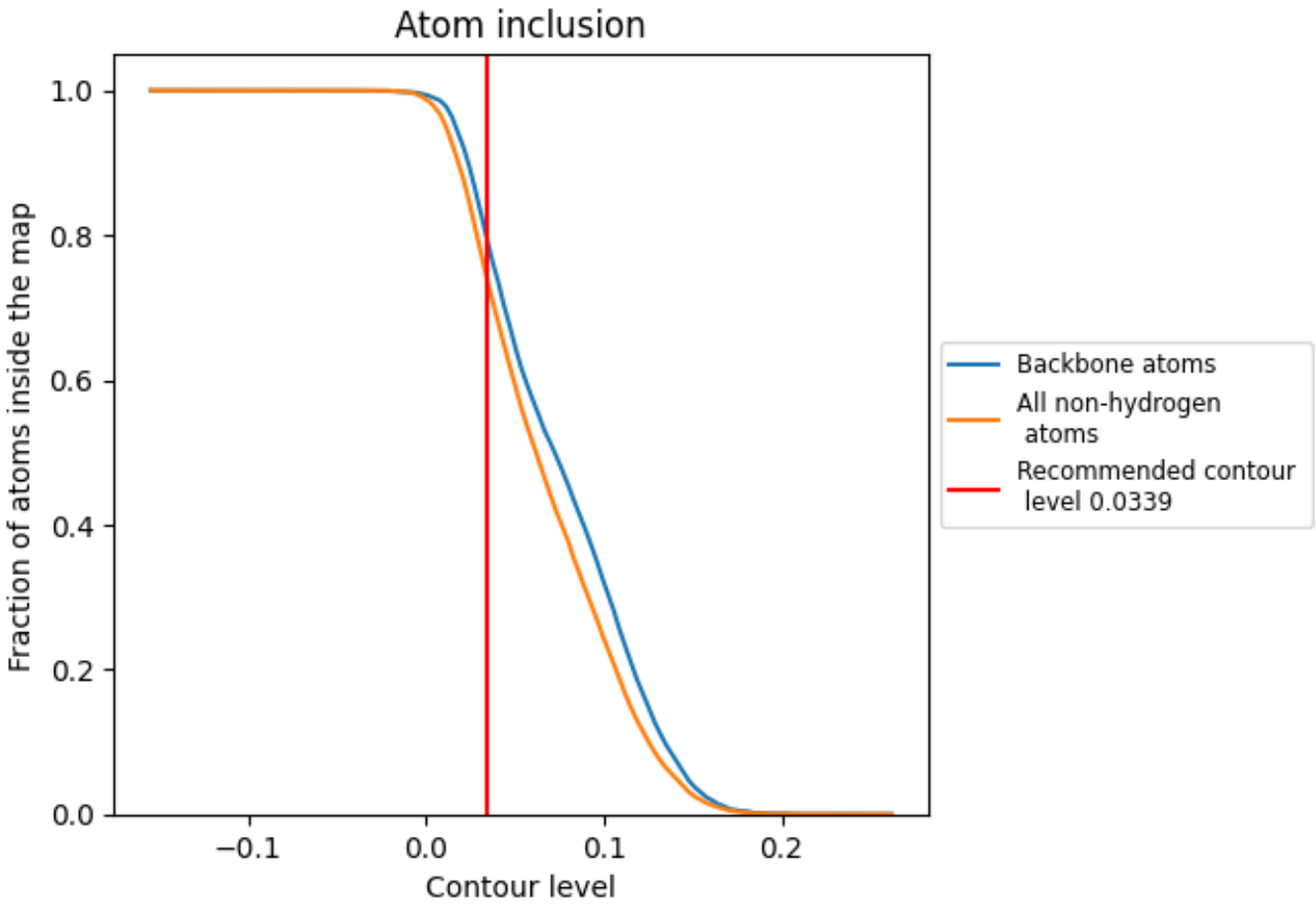
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model (i)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0339).

9.4 Atom inclusion (i)



At the recommended contour level, 80% of all backbone atoms, 74% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.0339) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7427	0.4970
A	0.8240	0.5400
B	0.7897	0.5140
C	0.8236	0.5290
D	0.5811	0.4290
E	0.4371	0.3760
H	0.7816	0.4980
L	0.7383	0.4970